

**Genetic Analysis of Bull Trout in the
Jarbidge River Watershed, Nevada/Idaho**

FINAL REPORT

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Summary

The Jarbidge River in Idaho and Nevada represents the southern-most habitat occupied by bull trout across the species range. Bull trout in the Jarbidge River have been isolated from other populations for over 100 years due to the construction of multiple impassable dams and several kilometers of unsuitable habitat. Given its unique geographic location and isolated nature, the conservation of bull trout populations in the Jarbidge River is a high priority. Although genetic data has been recognized as an important factor for guiding bull trout recovery planning in the Jarbidge River system, previously genetic information related to Jarbidge bull trout populations was limited. Our objective in this study was to provide a fine-scale analysis of genetic variation within and among Jarbidge bull trout populations. We used a suite of 15 microsatellite loci to characterize genetic variation within and among six tributaries in the Jarbidge River that contain bull trout. Estimates of genetic variation within these six populations including allelic richness and expected and observed heterozygosity tended to be lower than those we had observed for other populations across the species range. Estimates of effective population size were less than 50 individuals for all six of the tributary populations. Estimates of variation among populations indicated that each tributary contains a genetically distinct spawning population. The greatest level of variation we observed was between tributaries in the East and West Fork. We observed greater levels of gene flow among West Fork Jarbidge tributaries than we did among East Fork tributaries and little evidence for gene flow between the East and West Fork Jarbidge. Genetic population assignments suggest that individuals migrate among tributaries within the East and West Fork and to a lesser extent between the two forks.

Introduction

The Jarbidge River in southwest Idaho and northern Nevada is a tributary in the Snake River basin and contains the southernmost habitat currently occupied by bull trout (*Salvelinus confluentus*). This population segment is geographically separated from other bull trout in the Snake River basin by more than 240 kilometers (150 miles) of unsuitable habitat and several impassable dams on the mainstem Snake River and the lower Bruneau River. The Jarbidge River core area consists of the entire mainstem Jarbidge River and the East and West Forks of the Jarbidge River and their tributaries. The U.S. Fish and Wildlife Service (USFWS) draft recovery plan for bull trout in the Jarbidge River identifies six local populations within the Jarbidge River: the East Fork Jarbidge River (including the East Fork headwaters, Cougar Creek, and Fall Creek), Dave Creek, Slide Creek, West Fork Jarbidge River (including Sawmill Creek), Jack Creek, and Pine Creek (USFWS 2004; Figure 1). The geographic uniqueness of bull trout in the Jarbidge River, in addition to their physical isolation, potentially makes the Jarbidge River bull trout population a high conservation priority for maintaining genetic diversity and the evolutionary potential of the species.

The genetic consequences of population isolation and fragmentation have been previously documented for bull trout (Whitely et al. 2006; Costello et al. 2003; Nerass and Spruell 2001). Costello et al. (2003) demonstrated the effect of isolating populations above barriers on levels of genetic variation, however, none of these populations were as geographically isolated as the Jarbidge River populations. Fragmentation of populations via dams and other habitat alterations may result in genetic bottlenecks (Yamamoto et al. 2004), increased rates of inbreeding (Rieman and Allendorf 2001), and changes in life history (Morita et al. 2000).

Spruell et al. (2003) conducted a range-wide genetic survey of bull trout populations and suggested that bull trout populations in the Jarbidge River basin have a shared evolutionary history with populations in the upper Columbia River basin and upper Snake River basin. However, this study contained a relatively small sample size ($n = 37$) from the Jarbidge River system and did not investigate fine scale levels of population structure present within the Jarbidge River and its tributaries. Recently more polymorphic microsatellite markers have been developed for bull trout (e.g. DeHaan and

Ardren 2005) that allow for a more fine scale investigation of the population structure within the Jarbidge River system. Despite the evidence that historically there was some level of gene flow between the Jarbidge River population segment and bull trout in the Columbia River basin, bull trout in the Jarbidge River population segment have now been isolated from other populations for over 100 years (Gilbert and Evermann 1894).

Previously we examined levels of genetic variation within and among five bull trout spawning tributaries in the Jarbidge River system: Dave Creek, East Fork Jarbidge, Pine Creek, West Fork Jarbidge, and Jack Creek (DeHaan and Ardren 2007). Bull trout populations in the Jarbidge River had slightly lower levels of genetic diversity than those observed for other populations throughout the species range. The overall level of genetic variation among populations was consistent with observations from other river systems, including other populations within the Snake River system. Levels of gene flow were generally lowest between tributaries in the East and West Fork Jarbidge River and tended to be greater among populations within the two forks. Genetic assignment data from this study also suggested limited migration between the East and West Fork Jarbidge.

Following our previous report, additional sampling was conducted in the Jarbidge River system to increase sample sizes as well as the number of populations sampled. In this final report we build upon the results presented in DeHaan and Ardren (2007). Our primary objective was to finalize a baseline dataset used to characterize genetic variability and population structure among Jarbidge River bull trout populations. Additionally we wished to use the baseline dataset to examine patterns of fish movement within the Jarbidge River. Information generated from this study will be useful for developing conservation and management plans for bull trout in this isolated population.

Methods

Sample Collections

In 2006 and 2007 U.S. Geological Survey (USGS) personnel collected fin clips from bull trout captured in eight tributaries in the Jarbidge River system for the development of a baseline dataset: Dave Creek, East Fork Jarbidge, Slide Creek, Fall Creek, and Cougar Creek in the East Fork Jarbidge River and West Fork Jarbidge, Pine Creek, and Jack Creek in the West Fork Jarbidge River (Figure 1). Individuals were

collected via electrofishing and fin clips were taken for genetic analysis and preserved in 100% non-denatured ethanol. Individuals for genetic baseline collections ranged in size from 95-246mm fork length in 2006 and 55-247mm fork length in 2007. Additionally we received fin clips from 5 individuals collected in the East Fork Jarbidge River in 1999 and 10 individuals collected in Jack Creek in 1999. A number of bull trout that were collected did not fit the criteria for the baseline sampling protocol and fin clips from these individuals were used for genetic population assignments ($n = 34$ in 2006 and $n = 59$ in 2007). These fish were chosen for genetic assignments rather than baseline analysis because they were either 1) larger than 250mm (potentially migratory sub-adults or adults), 2) fish that were detected at PIT tag antennas, or 3) fish collected downstream of suspected spawning areas. These individuals ranged in size from 130-360mm in 2006 and 55-400mm in 2007.

Laboratory Analyses

Methods used to genotype the 2006 samples are outlined in DeHaan and Ardren (2007). DNA was extracted from all of the 2007 samples using a modified chelex extraction protocol (Miller and Kapuscinski 1996). All individuals were genotyped at a suite of 16 microsatellite loci; *Omm1128*, *Omm1130* (Rexroad et al. 2001), *Sco102*, *Sco105*, *Sco106*, *Sco107*, *Sco109*, (Washington Dept. of Fish and Wildlife *unpublished*), *Sco200*, *Sco202*, *Sco212*, *Sco215*, *Sco216*, *Sco218*, *Sco220* (DeHaan and Ardren 2005), *Sfo18* (Angers et al. 1995) and *Smm22* (Crane et al. 2004). PCR reactions were carried out in 10 μ l volumes containing 2 μ l of template DNA, 5 μ l of 2X QIAGEN Multiplex PCR Master Mix (final concentration of 3mM MgCl₂), and 0.2 μ l of oligonucleotide PCR primer mix. Primer mix compositions and annealing temperatures for each multiplex are given in Appendix 1. PCR conditions were as follows; initial denaturation at 95°C for 15 minutes, then 29 cycles of 95°C for 30 seconds, 90 seconds at the multiplex specific annealing temperature and 60 seconds primer extension at 72°C, followed by a final extension at 60°C for 20 minutes.

Following PCR, capillary electrophoresis was carried out on an ABI 3130xl Genetic Analyzer (Applied Biosystems Inc., Foster City, CA) according to the manufacturer's protocols. The G5 filter set was used to produce electropherograms, and

electrophoresis data was analyzed using the program Genemapper v4.0 (Applied Biosystems Inc.).

Statistical Analyses

Samples from 2006 and 2007 collected from the same tributary were combined for statistical analysis. Relatively few individuals were collected from two of the tributaries in this study; Cougar Creek (n=7) and Slide Creek (n=7). Because of the low sample sizes these two populations were omitted from the baseline analysis and instead these individuals were included in the group for genetic population assignments. The remaining samples were grouped according to their tributary of origin for statistical analysis.

Populations were tested for conformance to Hardy-Weinberg equilibrium (HWE) using the program GENEPOP v3.4 (Raymond and Rousset 1995). GENEPOP was also used to test each population for linkage disequilibrium. Significance values for HWE and linkage disequilibrium tests were adjusted for multiple comparisons using a sequential Bonferroni adjustment (Rice 1989). We used the program GDA (Lewis and Zaykin 2001) to estimate measures of genetic diversity including mean numbers of alleles per locus and observed and expected heterozygosity. In addition we used the program HP-Rare v1.0 (Kalinowski 2005) to estimate allelic richness for each population based on a minimum sample size of 66 genes (two times the minimum sample size). This program provides estimates of allelic richness that have been corrected for differences in sample size between populations. We performed a permutation test (1000 permutations) using the program FSTAT v2.9.3.2 (Goudet 2001) to test for significant differences in measures of genetic diversity between the East and West Fork. Populations were also tested for evidence of recent (within the past few generations) genetic bottlenecks using the program BOTTLENECK (Cornuet and Luikart 1996) assuming a two-phased model of mutation. This method tests for an excess of heterozygotes relative to allele the frequency of alleles in the population (Luikart and Cornuet 1998).

Previously we observed that a number of closely related individuals (i.e. full and half siblings) were collected in Dave Creek. To examine the level of relatedness in the Jarbidge River we estimated Queller and Goodnight (1989) coefficients of relatedness for

all pairs of individuals within each of the six tributaries using the program IDENTIX (Belkhir et al. 2002). The coefficient of relatedness (r_{xy}) ranges from -1.0 to 1.0 with a value of 0 indicating two individuals are no more related than the population average.

One important piece of information for developing effective management strategies for Jarbidge River bull trout populations that is currently lacking is the size of each local spawning population. Although we cannot provide population estimates using our dataset, genetic data can be used to provide estimates of effective population size (N_e). Effective population size can be defined as the size of an ideal population with the same rate of loss of genetic variation (genetic drift) as the population being studied (Allendorf and Luikart 2007). Although N_e is typically smaller than the true census population size, estimates of N_e can be used to make inferences about the number of adults spawning annually. Estimates of N_e were calculated based on linkage disequilibrium (Waples 2006) using the program LDNe v1.2 (Waples and Do 2008).

A number of different methods exist for determining the number of distinct populations present within a system (Waples and Gaggiotti 2006). We employed several of these methods to examine the level of genetic variation among the six spawning tributaries and to determine how many distinct spawning populations were present. We used FSTAT to estimate the overall level of genetic variation among all populations (F_{ST}) and the associated 95% confidence level based on 1000 bootstrap replicates. FSTAT was also used to estimate pairwise levels of genetic variation (F_{ST}) among all pairs of sampling locations and to test pairwise estimates for significance. Using GENEPOP, we performed a chi-squared contingency analysis to determine if there were significant differences in allele frequencies among the six spawning tributaries. P-values were adjusted for multiple comparisons using a sequential Bonferroni correction (Rice 1989) as well as the B-Y FDR correction described in Narum (2006).

The program Structure v2.2 (Pritchard et al. 2000) was also used to determine the most likely number of spawning populations that were present in the Jarbidge River system. This program uses a model-based clustering approach to determine the number of populations or clusters (K) that are present. Structure also gives the estimated membership of each individual in each of the K clusters. We performed 10 replicate unsupervised Structure runs for each K from 1-10. All runs had a burn-in of 30,000

iterations followed by 100,000 iterations. Two methods were used to infer the correct value of K for the dataset. Pritchard et al. (2000) showed that the posterior probabilities of K and Bayes' Rule can be used to estimate the correct value of K. This method simply identifies the K with the highest posterior probability for the dataset as the correct value of K. Evanno et al. (2005) suggested that the method of Pritchard et al. (2000) often leads to an over estimate of K and recommended using the second order rate of change between K and K+1 clusters, Delta K, as a more effective identifier of the correct K for the dataset. The symmetric similarity coefficient (SSC) was used to determine the similarity of outcomes among the 10 replicate Structure runs. We used the LargeKGreedy algorithm of CLUMPP (Jakobsson and Rosenberg 2007) with 1000 random input sequences to determine the number of distinct modes among the 10 runs.

We generated a neighbor-joining tree to examine the spatial relationship among spawning tributaries using the program Phylip v3.6 (Felsenstein 1993). The bootstrap procedure was used to generate 1,000 replicate datasets based on our observed allele frequencies. We then determined the Cavalli-Sforza and Edwards (1967) chord distance among the six tributaries and generated a consensus neighbor-joining tree based on these values.

Ninety-three individuals were collected in the Jarbidge River system for genetic population assignments. In order to assess our ability to correctly assign unknown fish to their population of origin we performed a jackknife analysis of our baseline dataset using the program WhichRun v4.1 (Banks and Eichert 2000). With this procedure each individual fish is removed from the baseline dataset and treated as an unknown. The allele frequencies for each population are then recalculated without that individual, and the individual is assigned to its most likely population of origin based on a maximum likelihood algorithm. The number of individuals that are assigned to their true population of origin provides a means of estimating the statistical power of the baseline dataset to assign unknown individuals. Once we had determined the ability of the baseline dataset to assign individuals, we used WhichRun to assign unknown fish to their first and second most likely population of origin. Confidence estimates for our assignments are represented by the likelihood ratio between the first and second most likely populations

(i.e. likelihood individual originated from population #1/likelihood individual originated from population #2).

Results

One locus, *Sfo18*, was fixed for a single allele in all six tributaries and *Sco102* was fixed for a single allele in all tributaries except for Pine Creek. Following Bonferroni correction, we observed a total of eight deviations from HWE out of a total of 85 tests. The locus *Sco109* deviated from HWE in Dave Creek and Fall Creek due to a deficiency of heterozygotes, and Jack Creek due to an excess of heterozygotes. Because this locus deviated from HWE in half of the populations, we excluded it from further analysis. Additionally, Dave Creek deviated from HWE at *Sco107* and *Smm22* due to a heterozygote deficiency, Fall Creek deviated from HWE at *Smm22* due to a heterozygote deficiency, Jack Creek deviated from HWE at *Sco200* due to a heterozygote excess and Pine Creek deviated from HWE at *Omm1128* due to a heterozygote deficiency.

We observed evidence of linkage disequilibrium in all populations. Pine Creek showed evidence of linkage at four pairs of loci, Dave Creek showed evidence of linkage at six pairs of loci, Fall Creek and West Fork Jarbidge showed evidence of linkage at eight pairs of loci, East Fork showed evidence of linkage at 11 pairs of loci and Jack Creek showed evidence of linkage at 30 pairs of loci. The pairs of linked loci appeared to be randomly distributed among the six tributaries.

Mean coefficients of relatedness were greater than 0 for all populations and were as follows: Dave Creek 0.170, East Fork 0.113, Fall Creek 0.260, Jack Creek 0.256, Pine Creek 0.118, and West Fork 0.157. The distribution of pairwise relatedness values was similar for Dave Creek, East Fork Jarbidge, Pine Creek, and West Fork Jarbidge (Figure 2). The distribution of pairwise relatedness values for Fall Creek and Jack Creek suggests that these populations had greater numbers of related individuals than the other populations in the Jarbidge River (Figure 2). Previously we adjusted the sample size in Dave Creek because a number of related individuals had been sampled (DeHaan and Ardren 2007). Relatedness estimates in the present analysis indicated that a number of full siblings had been sampled in the East Fork Jarbidge. These individuals were all collected from the furthest upstream sampling sites above an area that frequently goes

dry. These data suggest that only a single pair has reproduced in this section of the river recently and we removed all but one of the full siblings ($n = 12$) from the baseline dataset.

Estimates of genetic variation within populations varied somewhat among the six tributaries. Mean number of alleles per locus, allelic richness, expected and observed heterozygosity were all lowest in Jack Creek (3.800, 3.573, 0.430, 0.438 respectively). The mean number of alleles per locus was greatest in the East Fork Jarbidge and Pine Creek (5.133) and all other estimates of variation were greatest in East Fork Jarbidge (4.910, 0.515 and 0.506 for allelic richness, expected heterozygosity and observed heterozygosity respectively; Table 1). In general, measures of genetic variation within populations were slightly lower in the West Fork Jarbidge tributaries; however, we did not observe a significant difference in measures of genetic variation between the East Fork and the West Fork. None of the populations showed evidence of a recent genetic bottleneck. Estimates of N_e ranged from 3.4 for Jack Creek to 34.0 for Pine Creek (Table 2).

The overall level of genetic variation among populations (F_{ST}) was 0.116 and was found to be significantly different from zero. Pairwise estimates of F_{ST} ranged from 0.026 for the comparison between Pine Creek and West Fork Jarbidge to 0.206 for the comparison between Fall Creek and Jack Creek (Table 3). All pairwise estimates were found to be statistically significant. In general pairwise estimates of variation were greater for comparison between East and West Fork tributaries than comparison among populations within the East and West forks. We observed significant differences in allele frequencies among all population pairs. The neighbor-joining tree showed a split between the East Fork Jarbidge and West Fork Jarbidge tributaries (Figure 3). All branches on the tree showed greater than 50.0% bootstrap support. Within the West Fork Jarbidge, we observed that Pine Creek and West Fork Jarbidge were the most closely related and within the East Fork we observed that Fall Creek and Dave Creek were the most closely related.

The program structure was used to infer the most likely number of populations/clusters (K) in the Jarbidge River. Structure analysis showed that a K of 10 had the highest posterior probability for our dataset. Evanno et al. (2005) suggested that

simply looking at posterior probability often leads to an over estimate of K and recommended using the second order rate of change, Delta K, as a more effective identifier of the correct K for the dataset. When we used this method we found that a K of 6 was the most likely explanation for our dataset. The six populations/clusters identified by Structure generally corresponded to the six tributaries sampled for the baseline dataset (Figure 4). In the East Fork Jarbidge, the individuals from each tributary typically assigned to one specific cluster (i.e. the majority of the East Fork fish are shaded entirely orange). However, in the West Fork Jarbidge individuals within the three tributaries assign to multiple clusters (i.e. in Pine Creek both blue and grey individuals are present).

The proportion of individuals in the baseline dataset correctly assigned during the jackknife analysis ranged from 0.667 for Pine Creek to 1.000 for Dave Creek (Table 4). The proportion of individuals assigned to their tributary of collection in the East Fork was greater than 0.90 for all three tributaries (Table 4). In the West Fork Jarbidge the proportion of individuals assigned to their tributary of collection was generally lower (Table 4). Assignment of individuals to their fork of origin (East vs. West) was much more accurate; 152 of 155 (98.0%) individuals collected in the East Fork were assigned to East Fork tributaries and 159 of 162 (98.1%) individuals collected in West Fork tributaries were assigned to West Fork tributaries.

We performed genetic assignments for a total of 93 individuals that did not meet the sampling protocol for the baseline dataset; 38 collected in East Fork tributaries and 55 collected in West Fork tributaries. Of the 38 fish collected in the East Fork, 25 were assigned to the East Fork and 13 were assigned to the West Fork (Figure 5). Of the 55 fish collected in the West Fork, 52 were assigned to the West Fork and five were assigned to the East Fork (Figure 5). Fish selected for population assignments fit into three categories: fish that were detected at PIT tag antenna arrays ($n = 34$), fish that were collected furthest downstream of spawning areas ($n = 42$) and sub-adult and adult sized fish ($n = 17$). All but one of the PIT tag interrogated fish were collected in West Fork tributaries and the majority of them (25 of 34) were assigned to the tributary they were collected from (Table 5a). In the group of 42 fish collected downstream of spawning areas, we observed individuals assigned to each of the six baseline tributaries (Table 5b). In this group, 10 of 18 fish collected in East Fork Tributaries were assigned to West Fork

tributaries yet only 2 of 14 fish collected in West Fork tributaries were assigned to tributaries in the East Fork (Table 5b). In the group of 17 sub-adult and adult sized fish, individuals were assigned to every tributary except for Dave Creek. Although we had fewer fish in this group, the majority of the individuals were assigned to a tributary in the fork they were collected from (Table 5c).

Discussion

Hybridization with non-native brook trout, *Salvelinus fontinalis*, is thought to be a major threat to bull trout persistence throughout the species range (Rieman et al. 1997). While brook trout have been introduced into the Jarbidge River watershed in the past, self sustaining populations are not believed to have been established within bull trout habitat (USFWS 2004). In this study we genotyped over 400 individuals from throughout the Jarbidge River system and we did not find any evidence of hybridization with brook trout.

Genetic Variation Within Populations

Numbers of alleles and levels of heterozygosity that we observed in the present study were greater than those observed by Spruell et al. (2003) for a sample of bull trout from the Jarbidge River. This difference can be attributed to the difference in genetic markers used between the two studies; the previous study used markers developed primarily from other salmonids whereas the markers in this study were developed primarily from bull trout. Estimates of allelic richness that we observed in this study were slightly greater than those we observed for other bull trout populations in Southwest Idaho (Deadwood River, Boise River) and Southeast Oregon (Malheur River) using these same genetic markers (USFWS *unpublished data*). When compared to bull trout populations range-wide, estimates of allelic richness observed in the Jarbidge were close to the median value we observed for 75 populations throughout the species range (4.517). Estimates of observed and expected heterozygosity for the Jarbidge River were slightly lower than those we observed in other bull trout populations in Southwest Idaho and Southeast Oregon and tended to be lower than those we observed in other populations across the species range in the continental United States (USFWS *unpublished data*).

Reductions we observed in genetic diversity compared to other bull trout populations are likely the result of both historic and contemporary factors. The Jarbidge River is the southernmost habitat occupied by bull trout. Previous studies have documented reduced genetic variability in fish populations near the limits of species distributions presumably due to patterns of re-colonization following glacial retreat (Costello et al. 2003; Stamford and Taylor 2004). Whitely et al. (2006) found that levels of genetic variation within bull trout populations in the Boise River, another system near the southern distribution of bull trout, were among the lowest observed in a comparison of populations from across North America. Reductions in genetic variation can also be attributed to the fact that the Jarbidge River has been isolated from other bull trout populations for over 100 years due to the construction of multiple dams and several miles of unsuitable habitat. Reductions in genetic variation have been observed for salmonids, including bull trout, isolated above barriers (Costello et al. 2003; Wofford et al. 2005; Whitely et al. 2006).

Estimates of genetic variation and effective population size were lowest in Jack Creek. A culvert located near the mouth of Jack Creek from 1981 to 1997 likely limited the number of adults that could access spawning habitat in this tributary (USFWS 2004). Reductions in genetic variation we observed in Jack Creek are likely due in part to the fact that a limited number of individuals were spawning in Jack Creek during the time period the culvert was in place. Although this population (and all the other populations in our study) did not show evidence of a recent genetic bottleneck, Jack Creek may have undergone a genetic bottleneck shortly after the culvert was constructed and we are unable to detect it because of the time that has elapsed since the bottleneck occurred.

Estimates of N_e we observed in the six Jarbidge River tributaries were generally low (Table 2). Although it is difficult to establish threshold values for N_e , it has been suggested that N_e less than 50 individuals is cause for concern in the short term (Franklin 1980; Allendorf and Luikart 2007). Following this criteria, populations of bull trout in the Jarbidge River appear to be at an immediate risk of inbreeding depression. Rieman and Allendorf (2001) used computer simulations to examine the relationship between N_e and census population size in bull trout. These authors found that for bull trout, N_e ranged between 0.5 and 1 times the mean annual number of spawning adults. If this rule is

applied for populations in the Jarbidge River, under the best case scenario the number of annual spawning adults is below 50 in all local populations except for the East Fork Jarbidge. It is important to point out however, that Rieman and Allendorf (2001) also found that demographic and life history characteristics can greatly influence N_e in bull trout populations; therefore any inferences of census population size based on estimates of N_e for Jarbidge populations should be interpreted cautiously. Estimates of N_e were lowest for Fall Creek and Jack Creek suggesting very few fish spawn in these two tributaries each year. Increased levels of relatedness we observed among the juvenile fish sampled from these two populations (Figure 2) also support the idea that relatively few adults spawn in these tributaries annually. It has been suggested that connectivity among local populations is important for maintaining genetic diversity, particularly in instances where N_e is low (Rieman and Dunham 2000; Rieman and Allendorf 2001). Presently no permanent barriers (e.g. dams) separate bull trout spawning tributaries within the Jarbidge River and connectivity among local populations may help to buffer the effects of reduced levels of genetic diversity and low N_e .

Genetic Variation Among Populations and Patterns of Gene Flow

Bull trout generally show high levels of genetic differentiation among populations throughout their range (Spruell et al. 2003; Costello et al. 2003). The high level of genetic variation we observed among bull trout populations in the Jarbidge River ($F_{ST} = 0.116$) was consistent with observations from other bull trout populations across the species range. For example, we observed an overall F_{ST} estimate of 0.095 across a similar spatial scale for bull trout in the Malheur River system in Oregon, another Snake River tributary (DeHaan et al. 2007a). Recent range-wide genetic analyses for bull trout using these same microsatellite markers and mitochondrial DNA markers indicate that Jarbidge River bull trout are most closely related to other bull trout populations in Southeast Oregon and Southwest Idaho including the Malheur, Boise and Payette River systems (USFWS *unpublished data*).

We used a variety of methods to determine the number of local spawning populations present in the Jarbidge River basin. Estimates of variation (F_{ST}) were significantly different among all pairs of populations. Contingency analyses also

suggested that there were significant allele frequency differences among all six spawning tributaries. Furthermore, Structure analysis found that the model with six populations/clusters was the best fit for our dataset. These six populations/clusters generally corresponded to the six tributaries we sampled (Figure 4). Despite the relatively small spatial scale of the Jarbidge River compared to other watersheds that bull trout inhabit, these data suggest that each tributary contains a genetically distinct spawning population. Similar patterns of genetic population structuring have been documented in other watersheds that bull trout inhabit (Spruell et al. 1999; Whitely et al. 2006; DeHaan et al. 2007b).

Genetic data from this study suggest reduced levels of gene flow between populations in the East and West Fork Jarbidge River. Although all pairwise estimates of variation were significant, in some cases we observed twice as much variation between East and West Fork tributaries (e.g. Jack Creek and Fall Creek; $F_{ST} = 0.205$) as we did between tributaries within the East or West Fork (e.g. Fall Creek and East Fork; $F_{ST} = 0.116$). The East and West Fork tributaries also grouped separately on the neighbor-joining tree with strong bootstrap support (Figure 3). In the jackknife analysis we observed only six fish out of 305 that were assigned to a tributary in the opposite fork (Table 4). Furthermore, the plot from the Structure analysis showed very few fish collected in the East or West Fork that originated from a population/cluster associated with the opposite fork. Although there are no permanent barriers to migration between the East and West Fork Jarbidge and fish have been observed to move between the two forks, movement does not necessarily imply gene flow and our data suggest little gene flow occurs between the two forks.

We observed differing patterns of gene flow among tributaries within the East Fork and the West Fork. Within the East Fork Jarbidge, we observed little evidence of gene flow among the three tributaries. Jackknife analysis showed that in the East Fork Jarbidge, the proportion of individuals assigned to their tributary of origin was between 0.909 and 1.000. Furthermore, the Structure analysis indicated that there were three distinct clusters/populations within the East Fork and we observed very little mixing of individuals among the three clusters (e.g. individuals in Dave Creek are all shaded primarily red). Levels of gene flow appear to be greater among populations within the

West Fork Jarbidge. The pairwise estimates of F_{ST} we observed among West Fork tributaries were lower than those observed among East Fork tributaries in almost every instance (Table 3). The proportion of individuals correctly assigned to their tributary of origin in the jackknife analysis was also lower for the West Fork tributaries. The Structure plot shows that although there are three distinct clusters/populations among the West Fork tributaries, a number of individuals collected in each tributary assign to a different population (e.g. several individuals collected in Jack Creek assigning to the grey cluster associated with Pine Creek). Initial studies of fish movement in the Jarbidge using PIT tags confirm this pattern as more movement was observed among tributaries in the West Fork than in the East Fork; however antennas in the West Fork were better situated to detect movement into and out of tributaries (A. Taylor, USFWS, *personal communication*). Habitat differences between the East and West forks may explain the differences in levels of gene flow between the two forks. Spawning habitat within the East Fork is separated by a greater geographic distance than habitat in the West Fork making migration among spawning tributaries easier. Furthermore the quality of habitat in the East Fork remains relatively pristine whereas habitat in the West Fork has been disturbed to a greater extent due to construction of a road that runs along the river channel and the river flows through the town of Jarbidge. Increased rates of straying have been documented in other river systems where increased habitat disturbance has been observed (Quinn et al. 1991).

Our data suggest that the populations in Pine Creek and West Fork Jarbidge are very closely related. The pairwise F_{ST} estimate for these two populations (0.026) was nearly a third of our next lowest estimate (Pine and Jack Creek; 0.090). Pine Creek and West Fork Jarbidge populations grouped together with 93.0% bootstrap support on the neighbor-joining tree and the branch length between these two populations was much shorter, indicating a closer genetic relationship (Figure 3). When we assigned individuals from the baseline dataset to their most likely population of origin, 17 individuals collected in Pine Creek were assigned to tributaries other than Pine Creek with 11 of these 17 (65%) assigning to the West Fork Jarbidge. Although the majority (44 of 50) of the individuals collected in the West Fork Jarbidge were correctly assigned to the West Fork, all but one of the mis-assigned fish were assigned to Pine Creek. The geographic

proximity of these two tributaries is one explanation for their close relationship. Rearing habitat within these two streams is close to their confluence and juveniles may move between the two streams during rearing periods. Additionally, a seasonal barrier in the West Fork Jarbidge may have caused individuals that moved downstream of this barrier to migrate to Pine Creek when habitat above the barrier was inaccessible (B. Allen, USGS, *personal communication*).

Genetic Assignments and Patterns of Movement

Data from the 93 fish analyzed for population assignments suggest that although movement between the East and West Fork Jarbidge does occur, it is less common than movement among tributaries within the two forks. The majority of the individuals from both the East and West Fork were assigned to a tributary in the fork they were collected from (Figure 5). Approximately 66% of the fish analyzed for population assignments in the East Fork were assigned to tributaries in the East Fork, suggesting that approximately 34% of the fish analyzed for assignments in the East Fork were actually migrants from West Fork tributaries. In the West Fork Jarbidge, approximately 95% of the individuals analyzed for population assignments were assigned to West Fork tributaries suggesting that very few of the fish collected for assignments in the West Fork were migrants from East Fork tributaries. Similar to the baseline analysis, the genetic assignment data seem to suggest that individuals from West Fork Jarbidge tributaries migrate more than individuals from East Fork tributaries. Again, this may be the result of differences in habitat between the two forks (see above).

We found varying patterns of movement among the three classes of fish collected for population assignments. The majority (73.5%) of the 34 PIT tag interrogated fish were assigned to the tributary they were collected from and all but one of these fish were assigned to the fork they were collected from. Most of the PIT tag antennas were located near the mouths of the spawning tributaries and operated during times when fish typically move downstream to over-wintering habitat (A. Taylor, USFWS; B. Allen, USGS *personal communications*). The fact that most of these fish were assigned to the tributary they were collected from seems to suggest that they were detected while migrating downstream from natal rearing habitat or following spawning activity. We observed a

much lower correlation between capture location and genetic assignment location for the 42 individuals collected furthest downstream of spawning areas and the 17 individuals greater than 250mm (sub-adult and adult fish). During non-spawning periods bull trout are highly migratory (Brenkman et al. 2007; Downs et al. 2006; Muhlfeld et al. 2003). Although migration into and out of the Jarbidge River is not possible due to the presence of physical barriers downstream of the core area, there are no permanent barriers within the study area that would prevent fluvial bull trout from moving throughout the Jarbidge River core area. The population assignment data support the idea that bull trout in the Jarbidge system migrate among tributaries and even between the East and West Fork during non-spawning periods and that maintaining migratory corridors is important for bull trout in the Jarbidge system.

When considering the genetic population assignments, there are important caveats that should be considered when interpreting the results. Our ability to assign an individual to the correct tributary is often lower than our ability to assign an individual the correct fork (East vs. West). Because of this, some individuals may be mis-assigned to a tributary of origin but it is likely that they originated in the same fork as the tributary they were assigned to. For example, the jackknife analysis showed several fish collected in Pine Creek were assigned to other tributaries but most of were assigned to another West Fork tributary. The low number of fish collected in Slide Creek and Cougar Creek ($n = 7$ from each creek) prevented us from incorporating these populations into our genetic baseline. Because these populations were not in the baseline dataset used for assignments, individuals that originated in these two tributaries will always be assigned to a tributary they were not collected from. Given the level of differentiation between the East and West fork and the high accuracy of assignment to the correct fork, we presume that fish collected in tributaries not in the baseline would correctly assign to the East or West Fork.

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Table 1. Estimates of genetic variation within six bull trout populations in the Jarbidge River basin based on 15 microsatellite loci.

Population	n	A	A_r	H_{exp}	H_{obs}
<i>East Fork Jarbidge</i>					
Dave Cr.	63	4.000	3.734	0.468	0.452
E. Fork Jarbidge	59	5.133	4.910	0.515	0.506
Fall Cr.	33	4.133	4.133	0.457	0.440
Mean		4.422	4.259	0.480	0.466
<i>West Fork Jarbidge</i>					
Jack Cr.	61	3.800	3.555	0.427	0.438
Pine Cr.	51	5.133	4.799	0.486	0.501
W. Fork Jarbidge	50	4.267	4.089	0.482	0.498
Mean		4.400	4.148	0.465	0.479
Mean Over all Populations		4.411	4.203	0.472	0.473

A = Mean number alleles per locus

A_r = Allelic richness

H_{exp} = Heterozygosity expected

H_{obs} = Heterozygosity observed

Table 2. Estimates of effective population size (N_e) for six bull trout populations in the Jarbidge River basin. Estimates were calculated following the methods of Waples (2006).

Population	N_e	95% C.I.
Dave Cr.	11.8	7.7-17.3
E. Fork Jarbidge	34.0	22.6-56.5
Fall Cr.	7.2	4.0-10.4
Jack Cr.	3.4	2.8-4.8
Pine Cr.	22.3	16.5-30.8
W. Fork Jarbidge	14.8	11.7-18.7

Table 3. Pairwise estimates of genetic variation (F_{ST}) among six bull trout populations in the Jarbidge River based on 15 microsatellite loci.

	Dave Cr.	E. Fork Jarbidge	Fall Cr.	Jack Cr.	Pine Cr.	W. Fork Jarbidge
Dave Cr.	***					
E. Fork Jarbidge	0.097	***				
Fall Cr.	0.143	0.116	***			
Jack Cr.	0.108	0.137	0.206	***		
Pine Cr.	0.096	0.094	0.182	0.090	***	
W. Fork Jarbidge	0.124	0.105	0.169	0.114	0.026	***

Table 4. Jackknife assignment proportions for the Jarbidge River bull trout baseline dataset. Numbers in bold represent the proportion of individuals assigned to their capture location.

Collected From	Assigned to					
	Dave Cr.	E. Fork Jarbidge	Fall Cr.	Jack Cr.	Pine Cr.	W. Fork Jarbidge
<i>East Fork Tributaries</i>						
Dave Cr.	1.000	0.000	0.000	0.000	0.000	0.000
E. Fork Jarbidge	0.000	0.957	0.021	0.021	0.000	0.000
Fall Cr.	0.030	0.000	0.909	0.000	0.030	0.030
<i>West Fork Tributaries</i>						
Jack Cr.	0.000	0.000	0.000	0.918	0.049	0.033
Pine Cr.	0.039	0.020	0.000	0.059	0.667	0.216
W. Fork Jarbidge	0.000	0.000	0.000	0.020	0.100	0.880

Genetic Analysis of Bull Trout in the Jarbidge River

Table 5a. Genetic population assignments for 34 bull trout collected in the Jarbidge River that were also detected at PIT tag antenna arrays.

Collected From	Assigned to					
	Dave	E. Fork Jarbidge	Fall	Jack	Pine	W. Fork Jarbidge
<i>East Fork Tributaries</i>						
Dave	1					
E. Fork Jarbidge						
Fall						
<i>West Fork Tributaries</i>						
Jack		1		5	2	1
Pine				1	4	1
W. Fork Jarbidge				1	2	15

Table 5b. Genetic population assignments for 42 bull trout collected downstream of spawning areas in the Jarbidge River.

Collected From	Assigned to					
	Dave	E. Fork Jarbidge	Fall	Jack	Pine	W. Fork Jarbidge
<i>East Fork Tributaries</i>						
Cougar		2			1	2
Dave						
E. Fork Jarbidge		11		1		
Fall		2	2		1	
Slide		1		4	1	
<i>West Fork Tributaries</i>						
Jack		1		1	1	2
Pine	1				1	4
W. Fork Jarbidge					1	2

Table 5c. Genetic population assignments for 17 sub-adult and adult bull trout collected in the Jarbidge River.

Collected From	Assigned to					
	Dave	E. Fork Jarbidge	Fall	Jack	Pine	W. Fork Jarbidge
<i>East Fork Tributaries</i>						
Cougar		1				1
Dave						
E. Fork Jarbidge		4			1	
Fall					1	
Slide		1				
<i>West Fork Tributaries</i>						
Jack			1	1		1
Pine					2	
W. Fork Jarbidge		1				2

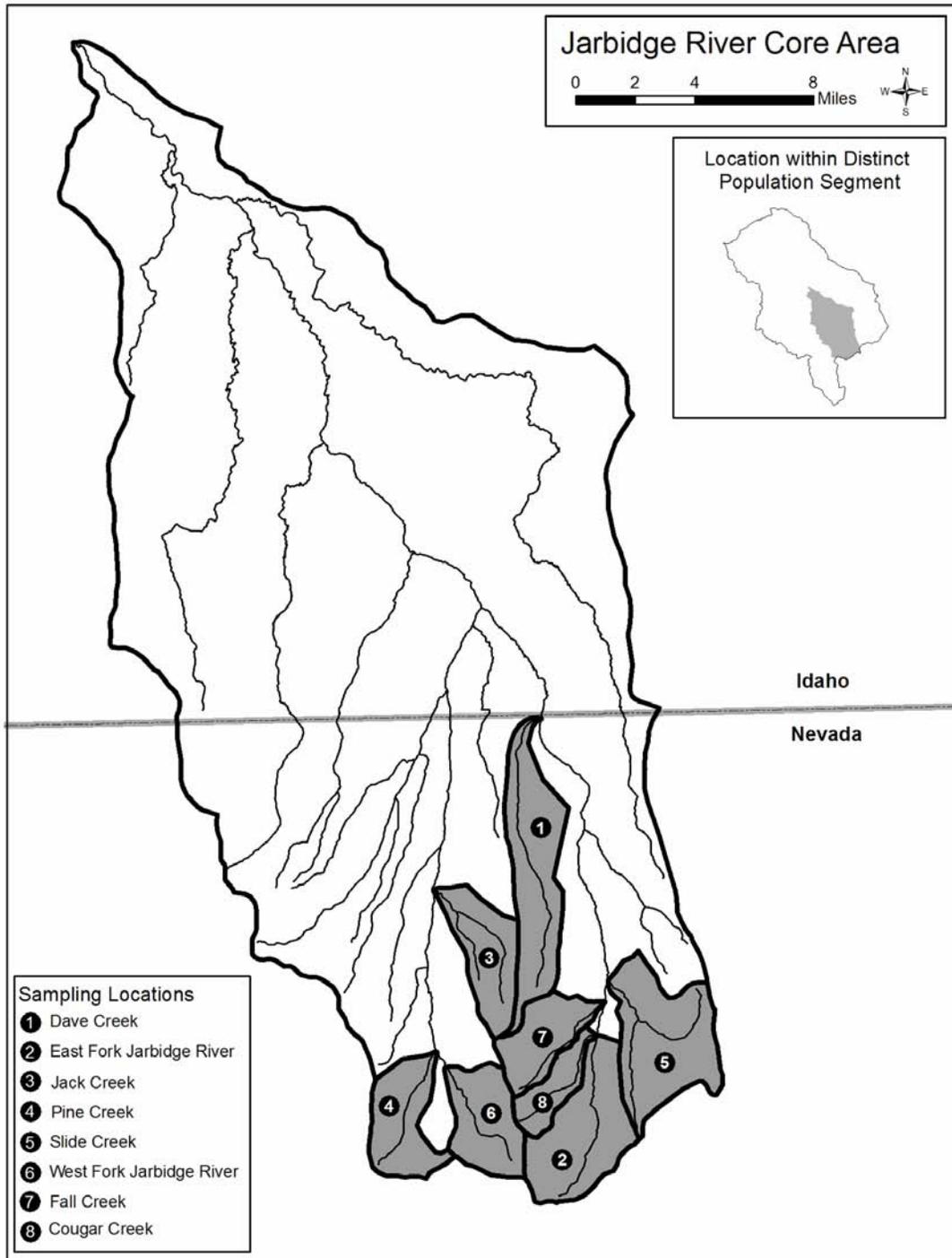


Figure 1. Jarbidge River basin in Idaho and Nevada. Sampling locations for bull trout are indicated by the shaded regions on the map.

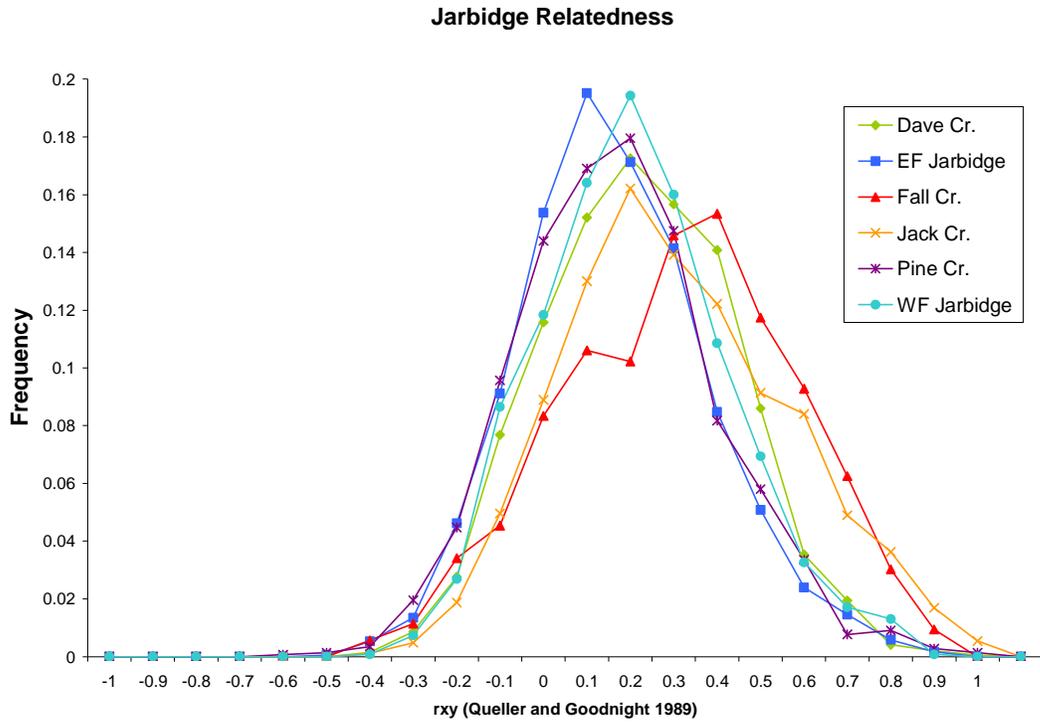


Figure 2. Distribution of pairwise coefficients of relatedness (r_{xy}) for six bull trout populations in the Jarbidge River basin. Values range from -1.0 to 1.0 with a value of 0 indicating a pair is no more related than the population average. The skew in the distribution for Fall Creek and Jack Creek suggest an increased number of related individuals in these two populations.

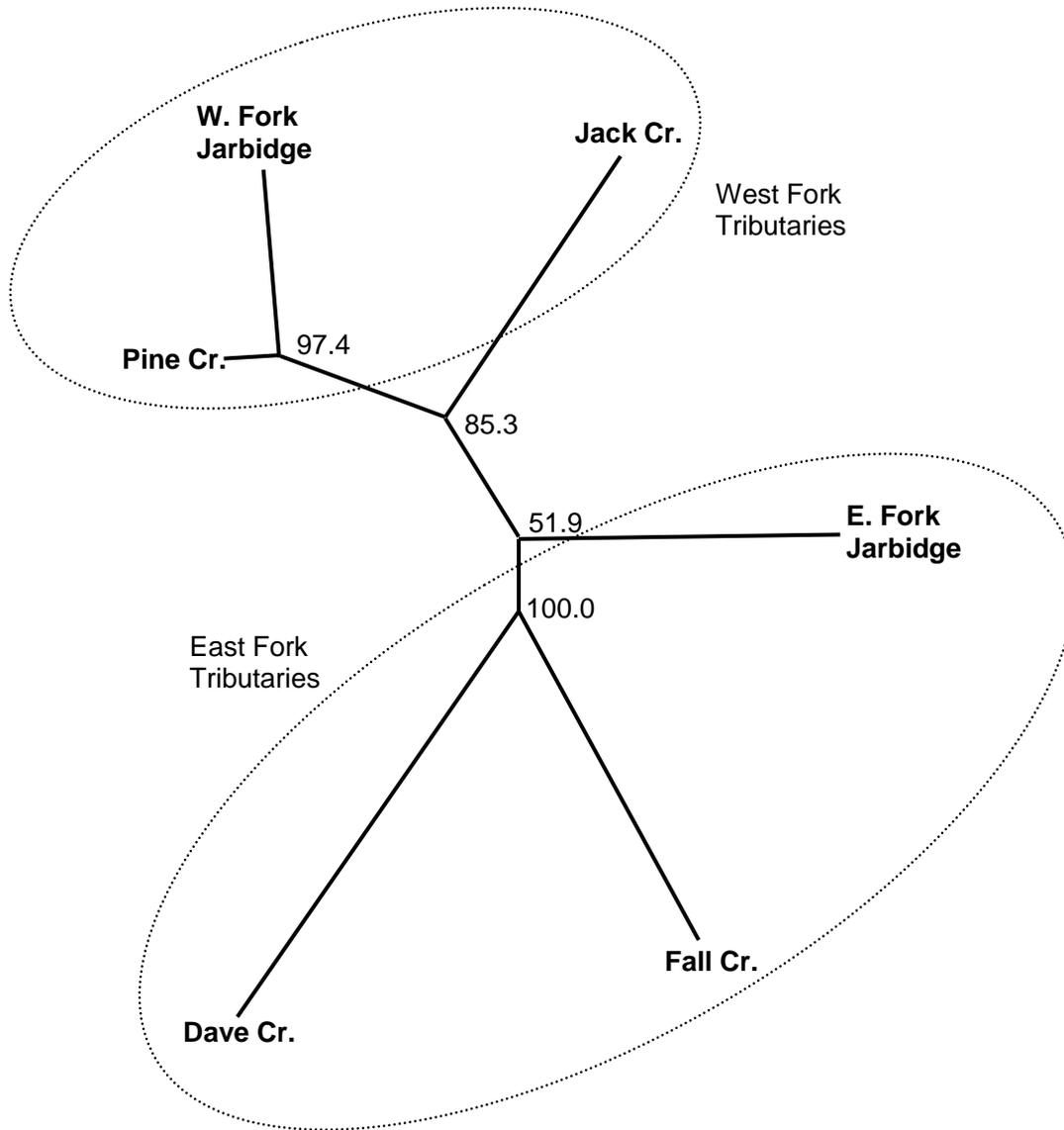


Figure 3. Neighbor-joining tree based on Cavalli-Sforza and Edwards chord distance for six bull trout populations in the Jarbidge River basin. Values on the nodes represent the percent of 1000 bootstrap replicates that displayed the given structure.

Jarbidge Bull Trout Structure Analysis K=6

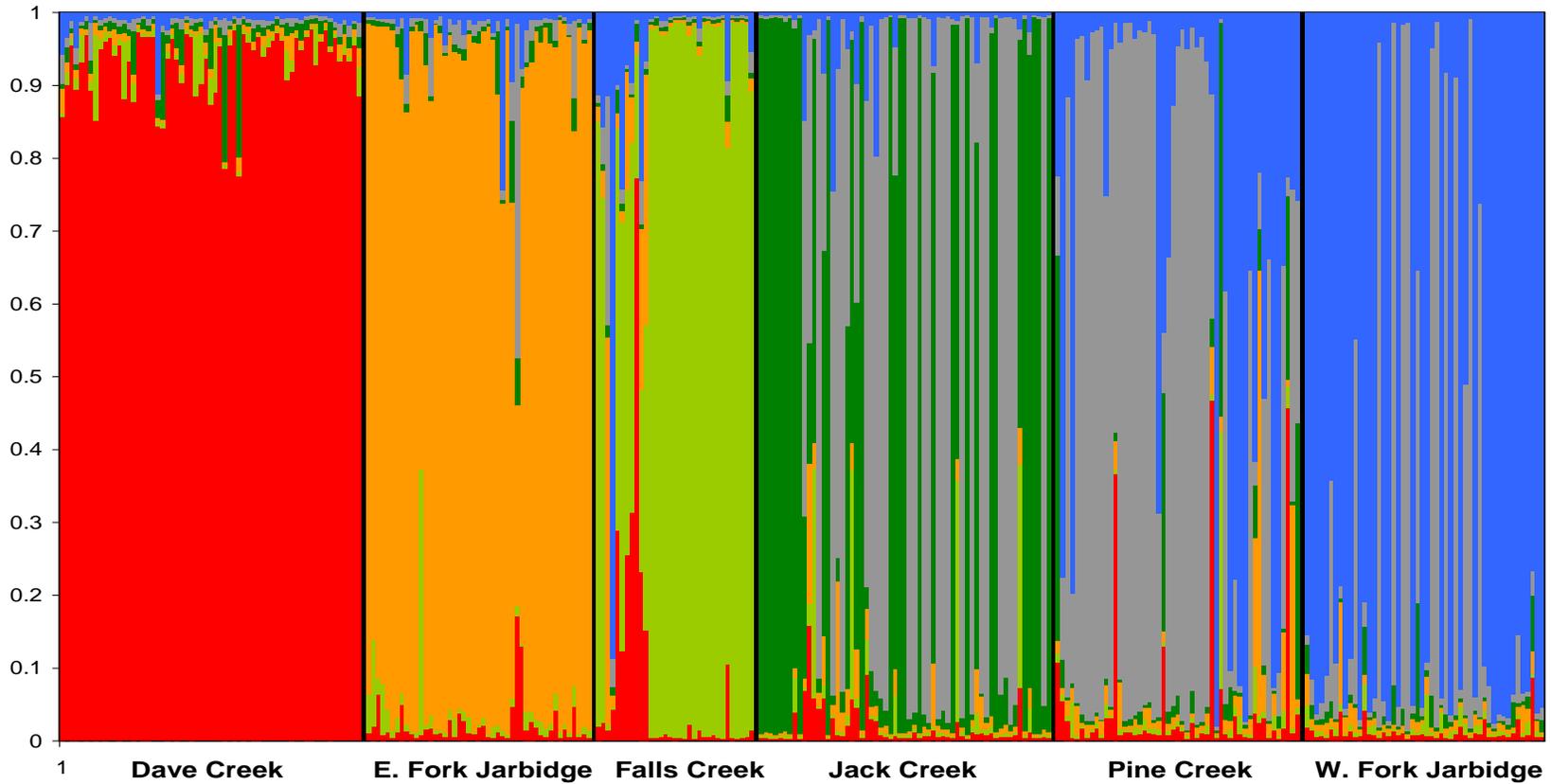


Figure 4. Output from the program Structure assuming $K=6$ inferred populations. Each vertical bar on the graph represents an individual fish in the baseline dataset. The colors on each bar represent the portion of each individual's genotype that originated from each of the six inferred population clusters.

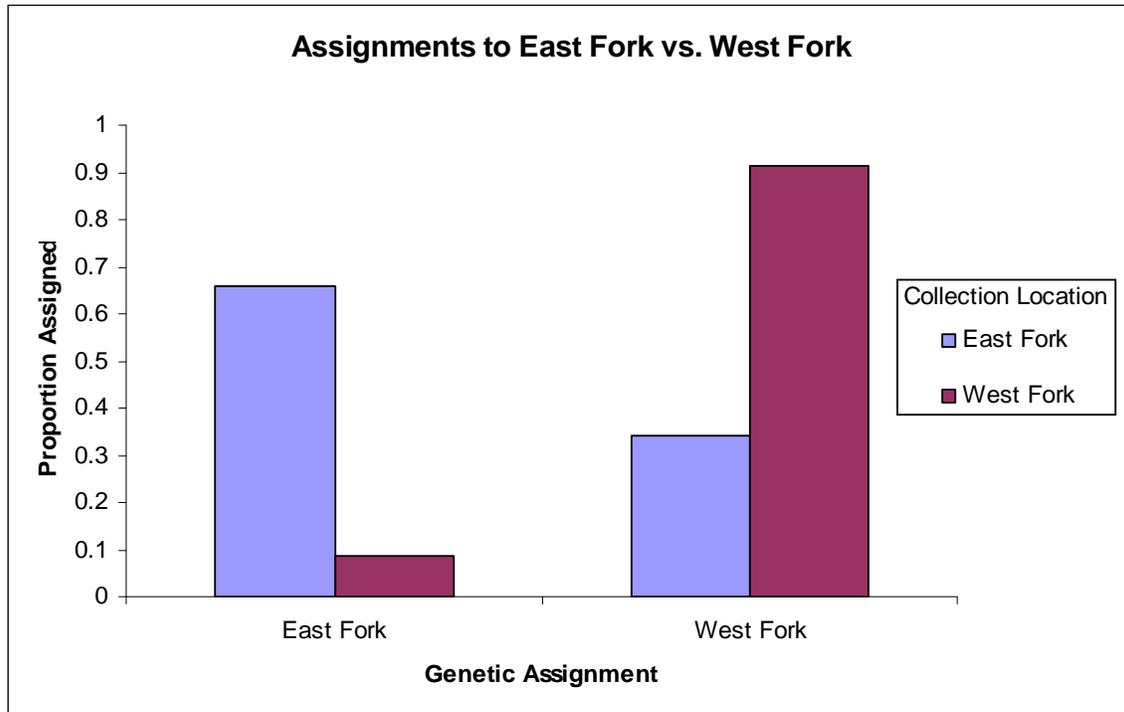


Figure 5. Genetic assignments to East vs. West Fork Jarbidge for 93 bull trout analyzed for population assignments in the Jarbidge River system.

Appendix 1. Bull trout PCR multiplex primer concentrations and annealing temperatures.

Multiplex Set 1 $T_A = 54^\circ\text{C}$

Locus Name	Dye	Final Concentration
Sfo18	6FAM	0.3 μM
Sco212	VIC	1.0 μM
Sco220	NED	3.3 μM
Sco216	PET	4.0 μM
Sco109	6FAM	6.6 μM

Multiplex Set 2 $T_A = 59^\circ\text{C}$

Locus Name	Dye	Final Concentration
Sco202	6FAM	0.6 μM
Sco102	PET	1.0 μM
Sco215	PET	1.3 μM
Sco200	VIC	2.0 μM
Omm1128	VIC	2.0 μM
Sco105	NED	1.3 μM
Smm22	6FAM	4.6 μM

Multiplex Set 3 $T_A = 56^\circ\text{C}$

Locus Name	Dye	Final Concentration
Sco106	6FAM	1.0 μM
Sco107	VIC	2.6 μM
Omm1130	NED	5.3 μM
Sco218	PET	3.3 μM

$T_A =$ Annealing temperature

Genetic Analysis of Bull Trout in the Jarbidge River

Appendix 2. Genetic population assignments for bull trout collected in the Jarbidge River. Colors for the individual ID numbers correspond to: Green = PIT tag interrogated fish; Blue = fish sampled downstream of spawning areas; Orange = Fish greater than 250mm fork length.

PIT Tag	ID	Capture Location	Most Likely Population #1	Likelihood Population #1	Most Likely Population #2	Likelihood Population #2	Likelihood Ratio*
3D9.1BF20B9DCF	JARB-171	WF Jarbidge	WF Jarbidge	4.00E+05	Pine Cr.	3.70E+04	10.979
3D9.1C2C465E26	1036-34	WF Jarbidge	WF Jarbidge	1.00E+04	Pine Cr.	56.76	182
3D9.1C2C4689DD	1009-032	WF Jarbidge	WF Jarbidge	3.00E+05	Pine Cr.	2.65E+03	120.5
3D9.1C2C4890A1	989-024	Dave Cr.	Dave Cr.	3.10E+04	EF Jarbidge	5.13695	6.01E+03
3D9.1C2C57345F	1009-019	Jack Cr.	WF Jarbidge	6.90E+04	Pine Cr.	9.97E+03	6.92665
3D9.1C2C57363E	989-093	EF Jarbidge	EF Jarbidge	241.9	WF Jarbidge	8.34149	29.005
3D9.1C2C57374D	989-090	EF Jarbidge	EF Jarbidge	1.60376	WF Jarbidge	0.0468234	34.251
3D9.1C2C574CDA	1009-001	Slide Cr.	EF Jarbidge	3.89832	Pine Cr.	0.0132594	294
3D9.1C2C574D10	1009-045	Pine Cr.	WF Jarbidge	5.30E+04	Pine Cr.	2.70E+04	1.98213
3D9.1C2C574D29	1036-003	Fall Cr.	Fall Cr.	668.6	Dave Cr.	57.704	11.587
3D9.1C2C574D5A	1009-028	WF Jarbidge	WF Jarbidge	1.00E+06	Pine Cr.	2.31E+03	536.7
3D9.1C2C57511F	989-095	EF Jarbidge	EF Jarbidge	1.23E+03	WF Jarbidge	0.00321919	4.00E+05
3D9.1C2C575249	989-100	EF Jarbidge	EF Jarbidge	1.85E+03	Pine Cr.	3.71676	498.9
3D9.1C2C575286	989-091	EF Jarbidge	EF Jarbidge	664.7	Fall Cr.	0.00329067	2.00E+05
3D9.1C2C575510	1009-036	WF Jarbidge	WF Jarbidge	4.00E+06	Pine Cr.	2.91E+03	1.35E+03
3D9.1C2C575670	1036-32	Slide Cr.	Pine Cr.	0.000514226	EF Jarbidge	0.000314913	1.63291
3D9.1C2C5757CB	1009-025	WF Jarbidge	Jack Cr.	3.14E+03	Pine Cr.	103.8	30.241
3D9.1C2C575A07	989-086	EF Jarbidge	EF Jarbidge	8.48E+03	Pine Cr.	0.00265098	3.00E+06
3D9.1C2C575B19	1009-018	Jack Cr.	Pine Cr.	1.64E+03	WF Jarbidge	0.268864	6.11E+03
3D9.1C2C575B46	1009-002	Slide Cr.	Jack Cr.	2.53E+03	Dave Cr.	192.5	13.126
3D9.1C2C575C87	1009-043	Pine Cr.	WF Jarbidge	207.4	Pine Cr.	45.361	4.57313
3D9.1C2C575D07	989-087	EF Jarbidge	EF Jarbidge	1.10E+04	Fall Cr.	0.14581	7.60E+04
3D9.1C2C575D80	989-083	EF Jarbidge	EF Jarbidge	49.176	Dave Cr.	1.40E-05	4.00E+06
3D9.1C2C575E99	989-085	EF Jarbidge	EF Jarbidge	174.3	WF Jarbidge	0.0492206	3.54E+03
3D9.1C2C575F6B	1009-047	Pine Cr.	WF Jarbidge	4.00E+04	Pine Cr.	5.53E+03	7.21921
3D9.1C2C576038	1009-026	WF Jarbidge	WF Jarbidge	7.83E+03	Pine Cr.	45.832	170.8
3D9.1C2C576079	1036-001	Fall Cr.	Pine Cr.	85.96	WF Jarbidge	66.898	1.28494
3D9.1C2C57616A	989-088	EF Jarbidge	Jack Cr.	759.8	Dave Cr.	233.9	3.24869
3D9.1C2C576338	1009-044	Pine Cr.	Jack Cr.	1.60E+04	Dave Cr.	3.77E+03	4.33794
3D9.1C2C5784E6	1009-038	WF Jarbidge	WF Jarbidge	67.129	Pine Cr.	2.39932	27.978
3D9.1C2C57927E	989-082	Cougar	EF Jarbidge	7.72E+03	Jack Cr.	31.247	247.1
3D9.1C2C579A65	989-084	EF Jarbidge	EF Jarbidge	749.2	Jack Cr.	0.0156587	4.80E+04
3D9.1C2C57E33E	1064-001	Jack Cr.	Jack Cr.	880.8	Dave Cr.	0.0803315	1.10E+04
3D9.1C2C57E377	1009-020	Jack Cr.	Jack Cr.	106.1	Dave Cr.	17.081	6.20986
3D9.1C2C57E5C4	1063-086	Pine Cr.	Pine Cr.	3.00E+05	EF Jarbidge	2.00E+05	1.38647
3D9.1C2C57E6C8	1009-048	Pine Cr.	Pine Cr.	9.32776	WF Jarbidge	0.0574003	162.5
3D9.1C2C57E86D	1036-002	Fall Cr.	Fall Cr.	26.765	Dave Cr.	1.03064	25.969
3D9.1C2C57E8DD	1009-035	WF Jarbidge	WF Jarbidge	5.00E+06	Pine Cr.	1.00E+05	34.526
3D9.1C2C5998F8	1009-040	WF Jarbidge	WF Jarbidge	8.60E+04	Pine Cr.	227.1	378.5
3D9.1C2C599B67	1009-057	Pine Cr.	Pine Cr.	1.00E+06	WF Jarbidge	2.10E+04	57.289
3D9.1C2C599CEA	1036-38	WF Jarbidge	WF Jarbidge	6.30E+04	Pine Cr.	39.301	1.59E+03
3D9.1C2C599CEC	1009-021	Jack Cr.	Pine Cr.	0.0975428	WF Jarbidge	4.44E-06	2.20E+04
3D9.1C2C599D47	1009-031	WF Jarbidge	WF Jarbidge	1.00E+06	Pine Cr.	2.30E+04	51.696
3D9.1C2C599DF2	1009-023	WF Jarbidge	WF Jarbidge	1.00E+05	Pine Cr.	9.00E+04	1.40521
3D9.257C59A600	1010-006	Cougar	WF Jarbidge	2.12E+03	Pine Cr.	712.7	2.97894
3d9.257C5A3D96	JARB-261	WF Jarbidge	EF Jarbidge	3.71935	Pine Cr.	0.481016	7.73228
3D9.257C5A416B	1009-037	WF Jarbidge	WF Jarbidge	6.40E+04	Pine Cr.	8.56E+03	7.44885

Genetic Analysis of Bull Trout in the Jarbidge River

PIT Tag	ID	Capture Location	Most Likely Population #1	Likelihood Population #1	Most Likely Population #2	Likelihood Population #2	Likelihood Ratio*
3D9.257C5A416B	JARB-265	WF Jarbidge	WF Jarbidge	6.40E+04	Pine Cr.	8.56E+03	7.44885
3D9.257C5A7510	JARB-199	Slide Cr.	EF Jarbidge	1.41485	Pine Cr.	1.55E-06	9.00E+05
3D9.257C5A8A95	1036-093	Jack Cr.	Fall Cr.	486.7	Jack Cr.	21.233	22.922
3D9.257C5AB8DA	JARB-053	WF Jarbidge	WF Jarbidge	7.85643	Fall Cr.	0.0158374	496.1
3D9.257C5AC17F	JARB-270	WF Jarbidge	Pine Cr.	22.685	Jack Cr.	0.496333	45.706
3D9.257C5AC601	JARB-267	WF Jarbidge	WF Jarbidge	389.3	Pine Cr.	42.371	9.18731
3D9.257C5AD026	JARB-067	Pine Cr.	Dave Cr.	537.7	Jack Cr.	135.8	3.96125
3D9.257C5AD7E1	1009-046	Pine Cr.	Pine Cr.	1.50E+04	WF Jarbidge	1.10E+04	1.34188
3D9.257C5AD7E1	JARB-079	Pine Cr.	Pine Cr.	1.50E+04	WF Jarbidge	1.10E+04	1.34188
3D9.257C5ADFBB	JARB-197	Slide Cr.	Jack Cr.	1.77E+03	Dave Cr.	320.4	5.51849
3D9.257C5AF5CE	JARB-175	EF Jarbidge	EF Jarbidge	17.636	Pine Cr.	0.00450873	3.91E+03
3D9.257C5B0ECF	JARB-066	Pine Cr.	WF Jarbidge	4.00E+06	Pine Cr.	1.00E+05	34.62
3D9.257C5B1253	JARB-189	Fall Cr.	EF Jarbidge	1.21E+03	WF Jarbidge	0.543038	2.24E+03
3D9.257C5B17B9	JARB-182	EF Jarbidge	EF Jarbidge	8.4269	Jack Cr.	1.02345	8.23381
3D9.257C5B1BBD	JARB-264	WF Jarbidge	Pine Cr.	24.86	Jack Cr.	8.36601	2.9715
3D9.257C5B1BD8	JARB-263	WF Jarbidge	WF Jarbidge	3.00E+05	Pine Cr.	1.00E+04	28.996
3D9.257C5B1C6A	JARB-275	WF Jarbidge	WF Jarbidge	0.0270864	Fall Cr.	0.000555778	48.736
3D9.257C5B1FCC	JARB-083	Pine Cr.	Pine Cr.	1.10E+04	WF Jarbidge	687.4	15.612
3D9.257C5B218F	JARB-174	EF Jarbidge	EF Jarbidge	1.10E+04	WF Jarbidge	0.596602	1.80E+04
3D9.257C5B2197	JARB-262	WF Jarbidge	Pine Cr.	1.00E+06	WF Jarbidge	42.152	2.80E+04
3D9.257C5B2197	1009-060	Pine Cr.	Pine Cr.	1.00E+06	WF Jarbidge	42.152	2.80E+04
3D9.257C5B2260	JARB-260	Jack Cr.	Jack Cr.	1.90E+04	Pine Cr.	865	22.051
3D9.257C5B22F3	JARB-212	Jack Cr.	WF Jarbidge	3.00E+06	Jack Cr.	3.00E+06	1.0488
3D9.257C5B27D2	JARB-247	Jack Cr.	Jack Cr.	7.54E+07	Pine Cr.	63.517	1.00E+06
3D9.257C5B2A21	JARB-200	Slide Cr.	Jack Cr.	2.40E+04	Dave Cr.	5.81E+03	4.10628
3D9.257C5B2A86	JARB-227	Jack Cr.	Jack Cr.	3.00E+05	Pine Cr.	494.9	615.9
3D9.257C5C903D	JARB-188	Fall Cr.	EF Jarbidge	923	Pine Cr.	5.86382	157.4
3D9.257C5CBCC1	JARB-240	Jack Cr.	Jack Cr.	8.00E+05	EF Jarbidge	0.565277	1.00E+06
3D9.257C5D17A4	JARB-218	Jack Cr.	Pine Cr.	33.45	Jack Cr.	21.472	1.55787
3D9.257C5D1BF3	JARB-198	Slide Cr.	Jack Cr.	3.16E+03	Fall Cr.	1.20E+03	2.62387
3D9.257C5D2B4A	1036-033	EF Jarbidge	Pine Cr.	13.196	Dave Cr.	12.839	1.02777
3D9.257C5D2B4A	JARB-194	Fall Cr.	Pine Cr.	13.196	Dave Cr.	12.839	1.02777
3D9.257C67F36C	JARB-202	Jack Cr.	EF Jarbidge	171.7	Fall Cr.	0.212785	806.8
3D9.257C67FFA4	1009-042	Pine Cr.	WF Jarbidge	287.5	Pine Cr.	2.23214	128.8
3D9.257C67FFA4	1036-37	WF Jarbidge	WF Jarbidge	287.5	Pine Cr.	2.23214	128.8
3D9.257C685E7D	1010-002	Cougar	EF Jarbidge	3.21E+03	Fall Cr.	32.399	99.026
3D9.257C687006	JARB-207	Jack Cr.	Jack Cr.	1.00E+07	Dave Cr.	1.76412	6.00E+06
3D9.257C6871EF	JARB-203	Jack Cr.	WF Jarbidge	5.86372	Pine Cr.	0.849628	6.90152
3D9.257C689B78	1010-003	Cougar	WF Jarbidge	1.85612	Jack Cr.	1.31017	1.41671
3D9.257C689DB3	1010-005	Cougar	Pine Cr.	0.00864783	EF Jarbidge	0.00489518	1.7666
3D9.257C689F8D	1010-004	Cougar	WF Jarbidge	4.32E+03	Pine Cr.	14.609	295.5
3D9.257C6CB18F	1010-001	Cougar	EF Jarbidge	2.00E+04	Jack Cr.	8.11E+03	2.48532
	JARB-201	Jack Cr.	EF Jarbidge	86.366	Pine Cr.	40.072	2.15528
	1009-022	Jack Cr.	WF Jarbidge	24.379	EF Jarbidge	4.08642	5.96588
	1010-063	EF Jarbidge	EF Jarbidge	501.7	Dave Cr.	2.9625	169.4
	1010-086	EF Jarbidge	EF Jarbidge	165.8	Fall Cr.	5.49897	30.159

* Represents the ratio of the likelihood of assigning to first most likely population/ the likelihood of assigning to second most likely population